ABSTRACT OF THE DISCLOSURE

Provided are nucleic acid coding sequences and methods utilizing these sequences for optimizing levels of substrates employed in the biosynthesis of copolymers of 3-hydroxybutyrate (3HB) and 3-hydroxyvalerate (3HV) in plants via manipulation of normal metabolic pathways using recombinant techniques. This optimization is achieved through the use of a variety of wild-type and/or deregulated enzymes involved in the biosynthesis of aspartate family amino acids, and wild-type or deregulated forms of enzymes, such as threonine deaminase, involved in the conversion of threonine to P(3HB-co-3HV) copolymer endproduct. These enzymes are used in conjunction with the E1α, E1β, E2, and E3 subunits of plastid pyruvate dehydrogenase complexes and branched chain oxoacid dehydrogenase complexes or mitochondrial dihydrolipoamide dehydrogenase E3 components to enhance the levels of threonine, 2-oxobutyrate (α-keto-butyrate), propionate, propionyl-CoA, β-ketovaleryl-CoA, and β-hydroxyvaleryl-CoA. Also provided are methods for the biological production of P(3HB-co-3HV) copolymer in plants utilizing the enhanced levels of propionyl-CoA produced therein. Introduction into plants of an appropriate β-ketothiolase, a β-ketoacyl-CoA reductase, and a PHA synthase in combinations with the aforementioned enzymes will permit such plants to produce commercially useful amounts of P(3HB-co-3HV) copolymers.